How to simulate alternative splicing?

I want to get Flux to simulate reads from different transcripts. So I am trying to understand how Flux deal with this situation. For example, if a gene has two isoforms. And an exon is absent in one isoform but present in the other. Those information are reflected in annotation file (gtf file). Therefore, how would Flux simulate reads which belong to that particular exon. Also will Flux generated reads across exon-exon boundary, this is to say the junction reads.